

SEQUENCE LISTING

SEQ ID NO: 1  
Sequence Length: 40  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG 40  
SEQ ID NO: 2  
Sequence Length: 39  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT 39  
SEQ ID NO: 3  
Sequence Length: 40  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGS GTTG 40  
SEQ ID NO: 4  
Sequence Length: 43  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG 43  
SEQ ID NO: 5  
Sequence Length: 40

0044001-12900

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGATTTC AGGTGCAGAT TWCAGCTTC

40

SEQ ID NO: 6

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGKTCY YTGYSAGYT YCTGRGG

37

SEQ ID NO: 7

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWWYCWG G

41

SEQ ID NO: 8

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGTGGGAY CTKTTTYCMM TTTTCAATT G

41

SEQ ID NO: 9

Sequence Length: 35

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

37

SEQ ID NO: 14  
Sequence Length: 36  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT 36  
SEQ ID NO: 15  
Sequence Length: 37  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAAGWTGT GGTAAACTG GGTTTTT 37  
SEQ ID NO: 16  
Sequence Length: 35  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGRAC TTG GGYTCAGCTT GRTTT 35  
SEQ ID NO: 17  
Sequence Length: 40  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCCTT 40  
SEQ ID NO: 18  
Sequence Length: 37  
Sequence Type: Nucleic acid

Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC 37  
SEQ ID NO: 19  
Sequence Length: 36  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT 36  
SEQ ID NO: 20  
Sequence Length: 33  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG 33  
SEQ ID NO: 21  
Sequence Length: 40  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG 40  
SEQ ID NO: 22  
Sequence Length: 37  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG 37

SEQ ID NO: 23

Sequence Length: 38

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGATTTCG GGCTGATTTT TTTTATTG 38

SEQ ID NO: 24

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG 37

SEQ ID NO: 25

Sequence Length: 28

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATCCCGGG CCACTGGATA GACAGATG 28

SEQ ID NO: 26

Sequence Length: 382

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

Clone: pUC-M21-V<sub>1</sub>

Features: 1..72 sig peptide

73..382 mat peptide

Sequence

ATG GAG TCA CAT ATT CAG GTC TTT GTA TAC ATG TTG CTG TGG TTG TCT	48
Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser	
5 10 15	

GGT GTT GAT GGA GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC	96
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser	
20 25 30	

ACA TCA GTA GGA GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT CAG AAT	144
Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn	
35 40 45	

GTG GGT ACT AAT GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT	192
Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro	
50 55 60	

AAA CCA CTG ATT TAC TCG GCA TCC TAT CGG TAC AGT GGA GTC CCT GAT	240
Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp	
65 70 75 80	

CGC TTC ACA GGC ACT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC ACC	288
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr	
85 90 95	

AAT GTG CAG TCT GAA GAC TTG GCA GAC TAT TTC TGT CAG CAA TAT AAC	336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn	
100 105 110	

AGC TAT CCT CGG CGG TTC GGT GGA GGC ACC AAA CTG GAA ATC AAA C	382
Ser Tyr Pro Arg Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
115 120 125	

SEQ ID NO: 27

Sequence Length: 409

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

Clone: pUC-M21-V<sub>II</sub>

Features: 1..57 sig peptide

58..409 mat peptide

Sequence

ATG AAA TGC AGC TGC GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG	48
Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly	
5 10 15	
GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGC GCA GAG CTT GTG AAG	96
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys	
20 25 30	
CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT	144
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile	
35 40 45	
AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG	192
Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu	
50 55 60	
GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC	240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp	
65 70 75 80	
CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA CCA GAC ACA TCC TCC AAC	288
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn	
85 90 95	
ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTG	336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val	
100 105 110	
TAT TAC TGT GCT TCG GCC TAC TAT GTT AAC CAG GAC TAC TGG GGT CAA	384
Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln	
115 120 125	



GGA ACC TCA GTC ACC GTC TCC TCA G

409

Gly Thr Ser Val Thr Val Ser Ser

130

135

SEQ ID NO: 28

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC

34

SEQ ID NO: 29

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGCGGATCCA CTCACGTTTG ATTCCAGTT TGGT

34

SEQ ID NO: 30

Sequence Length: 43

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT

43

SEQ ID NO: 31

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA

34

SEQ ID NO: 32  
Sequence Length: 18  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
CAGACAGTGG TTCAAACT 18

SEQ ID NO: 33  
Sequence Length: 26  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GAATTCGGAT CCACTCACGT TTGATT 26

SEQ ID NO: 34  
Sequence Length: 44  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC 44

SEQ ID NO: 35  
Sequence Length: 38  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG 38

SEQ ID NO: 36  
Sequence Length: 47  
Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG

47

SEQ ID NO: 37

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC

44

SEQ ID NO: 38

Sequence Length: 47

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG

47

SEQ ID NO: 39

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGTAGCTGT TATATTGCTG GCAGTAGTAG GTAGCGATGT CCTC

44

SEQ ID NO: 40

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

## Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21a-qk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

### Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
           -1  1                          5                          10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40

GTG GTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CGA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GCG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 41

Sequence Length: 31

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGTACCGACT ACACCTTCAC CATCAGCAGC C 31

SEQ ID NO: 42

Sequence Length: 31

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTGAAGGTG TAGTCGGTAC CGCTACCGCT A 31

SEQ ID NO: 43

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21b-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -3	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGT GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGC ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 44

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GCTACCTACT TCTGCCAGCA ATATAACAG  
SEQ ID NO: 45

29

Sequence Length: 29  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear

Molecular Type: Synthetic DNA  
Sequence  
TGCTGGCAGA AGTAGCTAGC GATGTCCTC  
SEQ ID NO: 46

29

Sequence Length: 379  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: Synthetic  
Original Source

Organism: Mouse and human  
Immediate Source

Clone: HEF-RVL-M21c-gx  
Amino acid -19--1:leader  
Amino acid 1 - 23:FR1  
Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

48

GTC GAC TCG GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG ACC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA GGA AAG GGT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCI CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 47

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21d-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1



Amino acid 24 - 34:CDR1  
 Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -3	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTC AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGG CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 48

Sequence Length: 29

Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

TGACAGAGTG TCCGTCACCT GTAAGGCCA

29

SEQ ID NO: 49

Sequence Length: 29

Sequence Type: Nucleic acid  
Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA  
Sequence

TTACAGGTGA CGGACACTCT GTCACCCAC

29

SEQ ID NO: 50

Sequence Length: 379

Sequence Type: Nucleic acid  
Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21e-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -3

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG CGC TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 51

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

00740073-122900

Clone: HEF-RVL-M21f-gx  
 Amino acid -19--1:leader  
 Amino acid 1 - 23:FR1  
 Amino acid 24 - 34:CDR1  
 Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAG TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GGC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	

09744873-122000

379

95

100

105

Topology: Linear

GACTTCACCT TGACCATCAG CAGCCT

26

Sequence Length: 26

Strandedness: Single

**Molecular Type:** Synthetic DNA

CTGCTGATGG TCAAGGTGAA GTCGGT

26

Sequence Length: 379

Strandedness: Double

**Topology:** Linear

**Molecular Type:** Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21g-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCG TTG GTA GGA ACA GGT AGA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCG 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asn Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GCG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 55

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

006221-2264260

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21h-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	

00749873-12900

CTC CAG CGA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 56

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCCGCT GATCTACTC 29

SEQ ID NO: 57

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCGGCT TTGGACTCTG TCCTGGCTT 29

SEQ ID NO: 58

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21i-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

00749873-12900



Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 59

Sequence Length: 26

Sequence Type: Nucleic acid

006221286460

Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GAGGACATCG CTGACTACTT CTGCCA  
SEQ ID NO: 60

26

Sequence Length: 26  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

AAGTAGTCAG CGATGTCCTC TGGCTG  
SEQ ID NO: 61

26

Sequence Length: 379  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: Synthetic  
Original Source

Organism: Mouse and human  
Immediate Source

Clone: HEF-RVL-M21j-gx  
Amino acid -19--1:leader  
Amino acid 1 - 23:FR1  
Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

48

00749873-12200

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GCG CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 62

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21k-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1  
 Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GGC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC GAG TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 63

Sequence Length: 379

Amino acid 98 - 107:FR4

CGG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

Immediate Source

Clone: HEF-RVL-M21m-gx  
 Amino acid -19--1:leader  
 Amino acid 1 - 23:FR1  
 Amino acid 24 - 34:CDR1  
 Amino acid 35 - 49:FR2  
 Amino acid 50 - 56:CDR2  
 Amino acid 57 - 88:FR3  
 Amino acid 89 - 97:CDR3  
 Amino acid 98 - 107:FR4

# Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CAA AAG TTC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATG ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAG TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAG AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	

0074003-12000

TAT CCT CGG GCG TTC GGC CAA GGG ACG AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

379

SEQ ID NO: 67

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCTGCT GATCTACTC

29

SEQ ID NO: 68

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCAGCTT TGGACTCTG TCCTGGCTT

29

SEQ ID NO: 69

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21n-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

006227-2266460



Amino acid 98 - 107:FR4

ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Ser	Leu	Val	Ala	Thr	Ala	Thr	Gly	
-19				-15					-10					-5		
GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
Val	His	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	
	-1		1					5					10			
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG	144
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val	
	15						20					25				
GGT	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	AGT	CCA	AAG	192
Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	
	30					35					40					
CTG	CTG	ATC	TAC	TCG	GCA	TCC	TAT	CGG	TAC	AGT	GGT	GTG	CCA	AGC	AGA	240
Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Ser	Arg	
45					50					55					60	
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TAC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
				65				70					75			
GTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAA	TAT	AAC	AGC	336
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	
			80					85					90			
TAT	CCT	CGG	CGC	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	C		379
Tyr	Pro	Arg	Ala	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys			
	95						100					105				

SEQ ID NO: 70

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M210-gr

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GGT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA CTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	

00744337-12-000000

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAG AGC 336  
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
           80                          85                          90

TAT CCT CGG GCG TTC GGC CAA CGG ACC AAG GTG GAA ATC AAA C 379  
 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
           95                          100                          105

SEQ ID NO: 71

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTCCAAAGC CGCTGATCTA CTC 23

SEQ ID NO: 72

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TAGATCAGCG GCTTTGGAGC CTT 23

SEQ ID NO: 73

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21p-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1



Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAGAAGCCTG	GGTCCTCAGT	GAAGTCTCC	TGCAAGGCTT	CTGGCTTCAA	CATTAAAGAC	60
ACCTATATAC	ACTGGGTGGC	CCAGGCTCCA	GGACAGGGCC	TGGAGTGGAT	GGGAAGGATT	120
CATCCTGAGG	ATGGTAA					137

SEQ ID NO: 75

Sequence Length: 111

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGAGATCTGA	GGACACAGCC	TTTTATTTCT	GTGCAAGTGC	CTACTATGTT	AACCAGGACT	60
ACTGGGCCCA	AGGCACCACT	GTACCCGTCT	CCTCAGGTGA	GTGGATCCGA	C	111

SEQ ID NO: 76

Sequence Length: 130

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACCTTCACTG	AGGACCCAGG	CTTCTTCACC	TCAGGTCGAG	ACTGCACCAG	CTGCACCTGG	60
GAGTGAGCAC	CTGGAGGTAC	AGCCAGCAAG	AAGAAGACCG	TCCAGGTCCA	GTCCATGGTC	120
GAAGCTTATC						130

SEQ ID NO: 77

Sequence Length: 132

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAAGGCTGTG	TCTTCAGATC	TCAGGCTGCT	GAGCTCCATG	TAGGCTGTGT	TCGTGATTG	60
GTCTGCAGTC	ATTGTCACTC	GCCCCTGGAA	CTTCGGGTCA	TATTTAGTAT	TACCATCCGC	120
AGGATCAATC	CT					132

SEQ ID NO: 78  
Sequence Length: 25  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GATAAGCTTC CACCATGGAC TGGAC

25

SEQ ID NO: 79  
Sequence Length: 25  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GTCGGATCCA CTCACCTGAG GAGAC

25

SEQ ID NO: 80  
Sequence Length: 409  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: Synthetic  
Original Source  
Organism: Mouse and human  
Immediate Source

Clone: HEF-RVH-M21-gy1  
Amino acid -19--1:leader  
Amino acid 1 - 30:FR1  
Amino acid 31 - 35:CDR1  
Amino acid 36 - 49:FR2  
Amino acid 50 - 66:CDR2  
Amino acid 67 - 98:FR3  
Amino acid 99 - 106:CDR3  
Amino acid 107 - 117:FR4

Sequence

**Topology:** Linear

### Sequence

60  
84

Sequence Length: 84

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

**Molecular Type:** Synthetic DNA

### Sequence

60  
84

SEQ ID NO: 83

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

**Topology:** Linear

**Molecular Type:** Synthetic DNA

### Sequence

CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG

34

SEQ ID NO: 84

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

**Topology:** Linear

**Molecular Type:** Synthetic DNA

### Sequence

CCACCCGAAC CACCACCACC TGAGGAGACG GTGACAGTGG T

41

SEQ ID NO: 85

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

**Molecular Type:** Synthetic DNA



### Sequence

GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G 41

SEO ID NO: 86

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

**Topology:** Linear

**Molecular Type:** Synthetic DNA

### Sequence

GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A 41

SEQ ID NO: 87

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

**Molecular Type:** Synthetic DNA

### Sequence

TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG 44

SEQ ID NO: 88

Sequence Length: 57

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

**Molecular Type:** Synthetic DNA

### Sequence

CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCTGA CCTTGGT 57

SEQ ID NO: 89

Sequence Length: 822

Sequence Type: Nucleic acid

Strandedness: Double

**Topology:** Linear

**Molecular Type:** Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: pSCFVT7-hM21

Amino acid 1 - 22:leader

Amino acid 23 - 139:H chain V region

Amino acid 140 - 154:Linker

Amino acid 155 - 261:L chain V region

Amino acid 262 - 269:FLAG

Amino acid sequence of Fv polypeptide scFv-hM21 and  
nucleotide sequence coding therefor

Sequence

ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT	48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala	
5 10 15	
GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG	96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu	
20 25 30	
GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC	144
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly	
35 40 45	
TTC AAC ATT AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA	192
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly	
50 55 60	
CAG GGC CTG GAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT	240
Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr	
65 70 75 80	
AAA TAT GAC CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA	288
Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu	
85 90 95	
TCC ACG AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC	336
Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp	
100 105 110	

ACA GCC TTT TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC Trp Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr 115 120 125	384
TGG GGC CAA GGG ACC ACT GTC ACC GTC TCC TCA GGT GGT GGT GGT TCG Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser 130 135 140	432
GGT GGT GGT GGT TCG GGT GGT GGC GGA TCG GAC ATC CAG ATG ACC CAG Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln 145 150 155 160	480
AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr 165 170 175	528
TGT AAG GCC AGT CAG AAT GTG GGT ACT AAT GTA GCC TCG TAC CAG CAG Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln 180 185 190	576
AAG CCA GGA AAG GGT CCA AAG CCG CTG ATC TAC TCG GCA TCC TAT CGG Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg 195 200 205	624
TAC AGT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp 210 215 220	672
TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr 225 230 235 240	720
TAC TGC CAG CAA TAT AAC AGC TAT GCT CGG GCG TTC GGC CAA GGG ACC Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr 245 250 255	768
AAG GTC GAA ATC AAA GAC TAC AAA GAC GAT GAC GAT AAA Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Lys 260 265	807
TAATAAGAAT TCTTG	822

SEQ ID NO: 90

Sequence Length: 45

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Features: Amino acid sequence of linker region of Fv polypeptide  
and nucleotide sequence coding therefor

Sequence

GGT GGT GGT GGT TCG GGT GGT GGT GGT TCG GGT GGT GGC GGA TCG

45

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

5

10

15

GGT GGT GGT GGT TCG GGT GGT GGT GGT TCG GGT GGT GGC GGA TCG  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser